

Claims:

- 5 1. A method of genotyping a nucleic acid sample comprising;
 (a) providing melt curves for a population of nucleic
acid samples hybridized to one or more nucleic acid probes;
 (b) applying one or more grouping lines to the population
of melt curves,
10 wherein each of the grouping lines intersects one or more
melt curves within said population,
 (c) assigning each said grouping line to a genotype
category, and;
 (d) determining the genotype category of a nucleic acid
15 sample in said population by identifying the grouping line
which intersects the melt curve of the sample.
2. A method according to claim 1 wherein said melt curves
are provided by
20 (a) contacting a population of nucleic acid samples with
one or more nucleic acid probes which hybridize with each of
the samples to form a population of complexes,
 (b) progressively altering the hybridization conditions
to decrease or increase the formation of said complexes;
25 (c) measuring output signals indicative of the extent of
hybridization of the complexes,
 (d) plotting changes in output signal relative to the
hybridization conditions for each of said population of
complexes to produce a population of melt curves.
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3. A method according to claim 1 or claim 2 wherein said
grouping lines are applied to said population of melt curves
by a user.

4. A method according to claim 3 wherein the user applies the grouping lines to a displayed image of said population of melt curves using a graphic interface.

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5. A method according to claim 1 or claim 2 wherein said grouping lines are applied to said population of melt curves by a data processor.

10 6. A method according to claim 5 wherein said grouping lines are applied by

(i) tracking the Y-value distribution of said melt curves along the X-axis,

(ii) identifying one or more regions in which said melt curves
15 separate into distinct clusters; and,

(iii) applying one or more grouping lines to define each said cluster.

7. A method according to claim 5 wherein said grouping lines
20 are applied by

(i) applying a plurality of candidate lines to said population of melt curves, and;

(ii)
identifying one or more candidate lines which only intersect a
25 discrete cluster of curves within said population as grouping lines.

8. A method according to any one claims 1 to 7 comprising;
applying a plurality of grouping lines to the population
30 of melt curves,

identifying one or more grouping lines intersected by the melt curve of the sample, and

applying an assignment algorithm to determine the genotype category of the nucleic acid sample.

9. A method according to claim 8 comprising;
5 assigning an order of precedence to the one or more grouping lines, and;
assigning the nucleic acid sample to the genotype category of the grouping line with the highest precedence.
- 10 10. A method according to any one claims 1 to 9 wherein the genotype category is selected from homozygous for sequences matched with an allelic reference sequence, homozygous for sequences mismatched with an allelic reference sequence, or
15 heterozygous.
11. A method according to any one of claims 1 to 10 wherein said melt curves plot changes in the output signal relative to the hybridization conditions.
- 20 12. A method according to any one of claims 1 to 10 wherein said melt curves plot the positive or negative first derivative of changes in the output signal relative to the hybridization conditions.
- 25 13. A method according to any one of the preceding claims comprising normalising said population of melt curves prior to applying said grouping lines.
14. A computer program product carrying computer-readable
30 code for performing the method of any one of claims 1 to 13.
15. Computer-readable code for performing the method of any one of claims 1 to 13.

16. A computer system configured to perform the method of any one of claims 1 to 13.
- 5 17. A DNA hybridization device having an output signal detector and a computer system according to claim 16 for analyzing data obtained by the detector.